

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Roger  
Bandman, Olga  
Wilde, Craig G.
- (ii) TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
  - (B) STREET: 3330 HILLVIEW AVENUE
  - (C) CITY: PALO ALTO
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Luther, Barbara J.
  - (B) REGISTRATION NUMBER: 33954
  - (C) REFERENCE/DOCKET NUMBER: PF-0027US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-855-0572

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: 223187
  - (B) CLONE: HUMAN PANCREAS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG 60  
GGGCTCACTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG 120  
ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA 180  
GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG 240  
GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGC 289

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUMAN PANCREAS
- (B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala 15  
1 5 10  
Phe Ser Pro Gln Gly Leu Thr Gly Pro Ala Ser Val Pro Thr Thr Cys 30  
20 25 30  
Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser 45  
35 40 45  
Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe 60  
50 55 60  
Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp 80  
65 70 75  
Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys 95  
85 90 95  
Pro

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUMAN PANCREAS

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCAGG      60
ACCCAAGGCA GTGATGGAGG GGCTCAGGAC TGTTGCCTCA AGTACAGCCA AAGGAAGATT      120
CCCGCCAAGG TTGTCCGCAG CTACCGGAAG CAGGAACCAA GCTTAGGCTG CTCCATCCCA      180
GCTATCCTGT TCTTGCCCCG CAAGCGCTCT CAGGCAGAGC TATGTGCAGA CCCAAAGGAG      240
CTCTGGGTGC AGCAGCTGAT GCAGCATCTG GACAAGACAC CATCCCCACA GAAACCAGCC      300
CAGGGCTGCA GGAAGGACAG GGGGGCCTCC AAGACTGGCA AGAAAGGAAA GGGCTCCAAA      360
GGCTGCAAGA GGAAGGACAG GGGGGCCTCC AAGACTGGCA AGAAAGGAAA GGGCTCCAAA      402
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUMAN PANCREAS

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
1          5          10          15
Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
20          25          30
Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
35          40          45
Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
50          55          60
Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
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65

70

75

80

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro  
85 90 95

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr  
100 105 110

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser  
115 120 125

Gln Thr Pro Lys Gly Pro  
130